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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=10; day=27; hr=10; min=3; sec=7; ms=792; ]

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Application No: 10588570 Version No: 1.0

**Input Set:**

**Output Set:**

**Started:** 2008-09-23 15:34:43.539  
**Finished:** 2008-09-23 15:34:46.103  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 564 ms  
**Total Warnings:** 37  
**Total Errors:** 8  
**No. of SeqIDs Defined:** 37  
**Actual SeqID Count:** 37

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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 342	'n' position not defined found at POS: 17 SEQID(5)
E 342	'n' position not defined found at POS: 18 SEQID(5)
E 342	'n' position not defined found at POS: 19 SEQID(5)
E 342	'n' position not defined found at POS: 20 SEQID(5)
E 342	'n' position not defined found at POS: 21 SEQID(5)
E 342	'n' position not defined found at POS: 22 SEQID(5)
E 342	'n' position not defined found at POS: 23 SEQID(5)
E 342	'n' position not defined found at POS: 24 SEQID(5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

**Input Set:**

**Output Set:**

**Started:** 2008-09-23 15:34:43.539  
**Finished:** 2008-09-23 15:34:46.103  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 564 ms  
**Total Warnings:** 37  
**Total Errors:** 8  
**No. of SeqIDs Defined:** 37  
**Actual SeqID Count:** 37

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Marx, Andreas  
Summerer, Daniel  
Rudinger, Nicolaus Zackes

<120> MUTATED DNA POLYMERASE WITH INCREASED MISPAIRING  
DISCRIMINATION

<130> 630196.401USPC

<140> 10588570  
<141> 2008-09-23

<150> PCT/EP2005/050479  
<151> 2005-02-04

<150> DE 102004005885.7  
<151> 2004-02-05

<160> 37

<170> PatentIn Ver. 2.1

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<213> Artificial Sequence

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<223> E. Coli wild type Klenow fragment of DNA polymerase I

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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> E.coli Klenow fragment of DNA polymerase I

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 20 25 30

Gly Glu Pro Thr Gly Ala Met Tyr Gly Val Leu Asn Met Leu Arg Ser  
 35 40 45

Leu Ile Met Gln Tyr Lys Pro Thr His Ala Ala Val Val Phe Asp Ala  
 50 55 60

Lys Gly Lys Thr Phe Arg Asp Glu Leu Phe Glu His Tyr Lys Ser His  
 65 70 75 80

Arg Pro Pro Met Pro Asp Asp Leu Arg Ala Gln Ile Glu Pro Leu His  
 85 90 95

Ala Met Val Lys Ala Met Gly Leu Pro Leu Leu Ala Val Ser Gly Val  
 100 105 110

Glu Ala Asp Asp Val Ile Gly Thr Leu Ala Arg Glu Ala Glu Lys Ala

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130	135	140	
Val Thr Pro Asn Ile Thr Leu Ile Asn Thr Met Thr Asn Thr Ile Leu			
145	150	155	160
Gly Pro Glu Glu Val Val Asn Lys Tyr Gly Val Pro Pro Glu Leu Ile			
165	170	175	
Ile Asp Phe Leu Ala Leu Met Gly Asp Ser Ser Asp Asn Ile Pro Gly			
180	185	190	
Val Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Leu Leu Gln Gly Leu			
195	200	205	
Gly Gly Leu Asp Thr Leu Tyr Ala Glu Pro Glu Lys Ile Ala Gly Leu			
210	215	220	
Ser Phe Arg Gly Ala Lys Thr Met Ala Ala Lys Leu Glu Gln Asn Lys			
225	230	235	240
Glu Val Ala Tyr Leu Ser Tyr Gln Leu Ala Thr Ile Lys Thr Asp Val			
245	250	255	
Glu Leu Glu Leu Thr Cys Glu Gln Leu Glu Val Gln Gln Pro Ala Ala			
260	265	270	
Glu Glu Leu Leu Gly Leu Phe Lys Lys Tyr Glu Phe Lys Arg Trp Thr			
275	280	285	
Ala Asp Val Glu Ala Gly Lys Trp Leu Gln Ala Lys Gly Ala Lys Pro			
290	295	300	
Ala Ala Lys Pro Gln Glu Thr Ser Val Ala Asp Glu Ala Pro Glu Val			
305	310	315	320
Thr Ala Thr Val Ile Ser Tyr Asp Asn Tyr Val Thr Ile Leu Asp Glu			
325	330	335	
Glu Thr Leu Lys Ala Trp Ile Ala Lys Leu Glu Lys Ala Pro Val Phe			
340	345	350	
Ala Phe Asp Thr Glu Thr Asp Ser Leu Asp Asn Ile Ser Ala Asn Leu			
355	360	365	
Val Gly Leu Ser Phe Ala Ile Glu Pro Gly Val Ala Ala Tyr Ile Pro			
370	375	380	
Val Ala His Asp Tyr Leu Asp Ala Pro Asp Gln Ile Ser Arg Glu Arg			
385	390	395	400
Ala Leu Glu Leu Leu Lys Pro Leu Leu Glu Asp Glu Lys Ala Leu Lys			
405	410	415	
Val Gly Gln Asn Leu Lys Tyr Asp Arg Gly Ile Leu Ala Asn Tyr Gly			

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435	440	445	
Leu Asn Ser Val Ala Gly Arg His Asp Met Asp Ser Leu Ala Glu Arg			
450	455	460	
Trp Leu Lys His Lys Thr Ile Thr Phe Glu Glu Ile Ala Gly Lys Gly			
465	470	475	480
Lys Asn Gln Leu Thr Phe Asn Gln Ile Ala Leu Glu Glu Ala Gly Arg			
485	490	495	
Tyr Ala Ala Glu Asp Ala Asp Val Thr Leu Gln Leu His Leu Lys Met			
500	505	510	
Trp Pro Asp Leu Gln Lys His Lys Gly Pro Leu Asn Val Phe Glu Asn			
515	520	525	
Ile Glu Met Pro Leu Val Pro Val Leu Ser Arg Ile Glu Arg Asn Gly			
530	535	540	
Val Lys Ile Asp Pro Lys Val Leu His Asn His Ser Glu Glu Leu Thr			
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565	570	575	
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580	585	590	
Lys Gln Gly Ile Lys Pro Leu Lys Lys Thr Pro Gly Gly Ala Pro Ser			
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610	615	620	
Lys Val Ile Leu Glu Tyr Arg Gly Leu Ala Lys Leu Lys Ser Thr Tyr			
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645	650	655	
Thr Ser Tyr His Gln Ala Val Thr Ala Thr Gly Arg Leu Ser Ser Thr			
660	665	670	
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675	680	685	
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690	695	700	
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770	775	780
Gln Lys Tyr Met Asp Leu Tyr Phe Glu Arg Tyr Pro Gly Val Leu Glu		
785	790	795
Tyr Met Glu Arg Thr Arg Ala Gln Ala Lys Glu Gln Gly Tyr Val Glu		
805	810	815
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Gln Gly Thr Ala Ala Asp Ile Ile Lys Arg Ala Met Ile Ala Val Asp		
850	855	860
Ala Trp Leu Gln Ala Glu Gln Pro Arg Val Arg Met Ile Met Gln Val		
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880		
His Asp Glu Leu Val Phe Glu Val His Lys Asp Asp Val Asp Ala Val		
885	890	895
Ala Lys Gln Ile His Gln Leu Met Glu Asn Cys Thr Arg Leu Asp Val		
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<223> Wildtype Taq polymerase

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 35 40 45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val

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115	120	125	
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210	215	220	
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225	230	235	240
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